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ANSWER 5 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 4

AN 1979:571063 CAPLUS  
DN 91:171063  
ED Entered STN: 12 May 1984  
TI Two-dimensional gel electrophoresis and  
computer analysis of proteins synthesized by clonal cell lines  
AU Garrels, James I.  
CS Neurobiol. Lab., Salk Inst., San Diego, CA, 92112, USA  
SO Journal of Biological Chemistry (1979), 254(16), 7961-77  
CODEN: JBCHA3; ISSN: 0021-9258  
DT Journal  
LA English  
CC 9-3 (Biochemical Methods)  
AB An improved method of 2-dimensional gel electrophoresis was developed  
which produced high resolution, reproducible images suitable for  
computer anal. In the images that were presented, >800 proteins  
were resolved without significant overlap, and many more proteins can be  
detected after longer exposures. To establish the usefulness of such  
methods for detailed quant. comparisons of cultured cells, extensive  
controls were carried out to test the reproducibility of the  
electrophoretic procedures, the same preparation procedures, and the cell  
culture conditions. A computerized scanning system was developed which  
can automatically detect and integrate the densities of the spots on a  
2-dimensional fluorogram or autoradiogram. The corresponding proteins  
from 2 samples can then be matched and their intensities compared.  
Several types of graphic output have been used to display the number and  
magnitude of the differences between the compared samples. These methods  
were used to study the patterns of protein synthesis in the nerve cell  
lines B103 and the glial cell line B9. Both exponentially  
dividing and stationary cultures were analyzed and the relative  
rates of synthesis of .apprx.300 proteins were compared by computer. For  
each cell line, no major qual. differences were found between  
dividing and stationary phase cells although numerous quant.  
differences of up to 15-fold were detected. When the 2 cell lines were  
analyzed in the same state of growth and compared by computer, qual.  
differences were found in .apprx.5% of the proteins analyzed, and  
≥40% of the shared proteins were involved in quant. differences of  
≥2-fold. The rates of synthesis of the shared proteins were more  
divergent between the 2 cell lines than between dividing and  
stationary phase cells of either line. Thus, these cell lines can be  
therefore be distinguished, regardless of growth state, by their  
cell-specific proteins and by their characteristic rates of synthesis of  
many of the shared proteins.  
ST protein electrophoresis nerve cell; glial cell protein electrophoresis  
IT Proteins  
RL: ANST (Analytical study)  
(electrophoresis of, of glial and nerve cell, computer application in)  
IT Computer application  
(in protein electrophoresis of glial and nerve cells)  
IT Nerve, composition  
Neuroglia  
(protein electrophoresis of cells of, computer application in)  
IT Electrophoresis and Ionophoresis  
(gel, of proteins, on polyacrylamide, computer application in)

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ST protein electrophoresis nerve cell; glial cell protein electrophoresis  
IT Proteins  
RL: ANST (Analytical study)  
(electrophoresis of, of glial and nerve cell, computer application in)  
IT Computer application  
(in protein electrophoresis of glial and nerve cells)  
IT Nerve, composition  
Neuroglia  
(protein electrophoresis of cells of, computer application in)  
IT Electrophoresis and Ionophoresis  
(gel, of proteins, on polyacrylamide, computer application in)

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DUPLICATE 4

AN 1991:45325 BIOSIS  
DN PREV199191023606; BA91:23606  
TI UV IMAGING DENSITOMETRY OF UNSTAINED GELS FOR TWO-DIMENSIONAL  
ELECTROPHORESIS.  
AU YAMAMOTO H [Reprint author]; NAKATANI M; SHINYA K; KIM B-H; KAKUNO T  
CS SHIMADZU CORP, NAKAGYO-KU, KYOTO 604, JPN  
SO Analytical Biochemistry, (1990) Vol. 191, No. 1, pp. 58-64.  
CODEN: ANBCA2. ISSN: 0003-2697.  
DT Article  
FS BA  
LA ENGLISH  
ED Entered STN: 10 Jan 1991  
Last Updated on STN: 10 Jan 1991  
AB A system suitable for ultraviolet imaging densitometry of two-dimensional  
electrophoretic gels that are unstained is described, together with its  
applications. A flying-spot densitometer linked with a personal  
computer was used for data acquisition, generation of mapping data,  
and image processing. Randomly distributed zones of proteins on  
two-dimensional gels were detected at 280 nm  
without being stained by two-dimensional scanning, and the densitometric  
value of each pixel (0.2 + 0.2 mm) was memorized by the  
computer, which generated a mapping pattern with density contours.  
The amount and densitometric value of cytochrome c had a linear  
relationship in the range of 2-200 µg. Zone locations of bovine linear  
proteins separated on two-dimensional gels  
were indicated on a map expressed in X-Y coordinates, and the pIs and  
molecular weights could be calculated from the map by use of pI and  
molecular weight markers on the same gel.  
CC General biology - Information, documentation, retrieval and computer  
applications 00530  
Biochemistry methods - Proteins, peptides and amino acids 10054  
Biochemistry studies - Proteins, peptides and amino acids 10064  
Biophysics - Methods and techniques 10504  
IT Major Concepts  
Biochemistry and Molecular Biophysics; Computer Applications  
(Computational Biology); Methods and Techniques  
IT Miscellaneous Descriptors  
PROTEINS COMPUTER ANALYSIS

AN 1982:16881 CAPLUS  
 DN 96:16881  
 ED Entered STN: 12 May 1984  
 TI The TYCHO system for computer analysis of two-dimensional gel electrophoresis patterns  
 AU Anderson, N. L.; Taylor, J.; Scandora, A. E.; Coulter, B. P.; Anderson, N. G.  
 CS Div. Biol. Med. Res., Argonne Natl. Lab., Argonne, IL, 60439, USA  
 SO Clinical Chemistry (Washington, DC, United States) (1981), 27(11), 1807-20  
 CODEN: CLCHAU; ISSN: 0009-9147  
 DT Journal  
 LA English  
 CC 9-7 (Biochemical Methods)  
 AB A computer system for the anal. of high-resolution 2-dimensional gel-electrophoresis patterns, and some initial applications are described. The system (called TYCHO) comprises programs for image acquisition, background subtraction and smoothing, spot detection, gaussian spot modeling, and pattern matching and comparison. It is based on a conventional minicomputer, but makes extensive use of a high-speed array processor in the image-processing and -modeling steps. Used in concert with the ISO-DALT 2-dimensional electrophoresis system (Anderson, N. G.; Anderson, N. L., 1978), TYCHO allows quant. measurement of hundreds of proteins in complex biol. samples, and constitutes the initial data-reduction system required for work towards a Human Protein Index.  
 ST protein electrophoresis computer analysis  
 IT Proteins  
 RL: ANST (Analytical study)  
 (electrophoresis of, computer anal. of)  
 IT Electrophoresis and Ionophoresis  
 (of proteins, computer anal. of)  
 IT Computer application  
 (to electrophoresis of proteins)

ANSWER 6 OF 7 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 3

AN 1982:213710 CAPLUS

DN 96:213710

ED Entered STN: 12 May 1984

TI Some relatively simple steps toward a computer system for the  
analysis of two-dimensional gel  
-electrophoresis autoradiographs

AU Fox, Stanley H.

CS Med. Cent., Univ. Cincinnati, Cincinnati, OH, 45267, USA

SO Clinical Chemistry (Washington, DC, United States) (1982), 28(4, Pt. 2),  
932-4

CODEN: CLCHAU; ISSN: 0009-9147

DT Journal

LA English

CC 9-7 (Biochemical Methods)

Section cross-reference(s): 80

AB A computerized system for the quant. comparison of 2-dimensional  
polyacrylamide gel autoradiographs is being developed that requires  
relatively limited hardware resources. Two fast, simple, and stable  
programs, one for background and streak subtraction and one for  
peak detection, were developed and tested. Two methods developed by  
others, one for image smoothing and one for peak matching, also  
were tested. A very simple spot-d. integration program that works on  
isolated spots has been written and is being developed further.

ST polyacrylamide gel autoradiog computer analysis; electrophoresis  
autoradiog computer analysis; protein electrophoresis autoradiog  
computer

IT Proteins

RL: ANT (Analyte); ANST (Analytical study)

(determination of, by 2-dimensional gel electrophoresis and autoradiog.,  
computerized anal. of)

IT Computer application

(in proteins determination by 2-dimensional gel electrophoresis and  
autoradiog.)

IT Radiography

(auto-, of proteins, after 2-dimensional gel electrophoresis,  
computerized anal. of)

IT Electrophoresis and Ionophoresis

(gel, two-dimensional, of proteins, autoradiog. combined with,  
computerized anal. of)

ANSWER 6 OF 7 CAPLUS COPYRIGHT 2006 ACS on STN. DUPLICATE 3

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ED Entered STN: 12 May 1984

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isolated spots has been written and is being developed further.

ST polyacrylamide gel autoradiog computer analysis; electrophoresis  
autoradiog computer analysis; protein electrophoresis autoradiog  
computer

IT Proteins

RL: ANT (Analyte); ANST (Analytical study)

(determination of, by 2-dimensional gel electrophoresis and autoradiog.,  
computerized anal. of)

IT Computer application

(in proteins determination by 2-dimensional gel electrophoresis and  
autoradiog.)

IT Radiography

(auto-, of proteins, after 2-dimensional gel electrophoresis,  
computerized anal. of)

IT Electrophoresis and Ionophoresis

(gel, two-dimensional, of proteins, autoradiog. combined with,  
computerized anal. of)

ANSWER 4 OF 5 JAPIO (C) 2006 JPO on STN

AN 1986-129562 JAPIO

TI QUANTITATIVE COMPARISON DEVICE FOR MIGRATION IMAGE

IN NISHINE TSUTOMU

PA SHIMADZU CORP

PI JP 61129562 A 19860617 Showa

AI JP 1984-251401 (JP59251401 Showa) 19841128

PRAI JP 1984-251401 19841128

SO PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined Applications, Vol. 1986

IC ICM G01N027-26

ICS G01N021-17

AB PURPOSE: To measure quantitatively protein components with high accuracy by using the migration spot of a protein component having a known migration pattern as a reference, comparing the protein component having an unknown migration pattern in a vital sample with the reference.  
CONSTITUTION: A two-dimensional migration gel 4 in which the protein components are migrated is divided to, for example, 4 regions 10a, 10b, 10c, 10d by isoelectric points. The standard material having the known migration pattern and mol. weight, for example, albumin, globulin or the like is preliminarily introduced into the gel 4. The standard material is measured, then the sample is measured in the optical concentration measurement. The variance in the dissipation quantity of the protein component dissipated from the two-dimensional gel by the gel equilibrating operation and gel dyeing operation after the end of the two-dimensional electrophoresis is thereby corrected and the quantitative comparison of the protein component in the same quantity of the sample migrated in the different two-dimensional gel is made possible.

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ANSWER 4 OF 5 JAPIO (C) 2006 JPO on STN

AN 1986-129562 JAPIO  
TI QUANTITATIVE COMPARISON DEVICE FOR MIGRATION IMAGE  
IN NISHINE TSUTOMU  
PA SHIMADZU CORP  
PI JP 61129562 A 19860617 Showa  
AI JP 1984-251401 (JP59251401 Showa) 19841128  
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DUPLICATE 3

AN 1990:371554 BIOSIS

DN PREV199090058235; BA90:58235

TI A REVIEW OF THE CLIP SYSTEM FOR THE QUANTITATIVE ANALYSIS OF  
TWO-DIMENSIONAL ELECTROPHORESIS GELS.

AU POTTER D J [Reprint author]

CS DEP ELECTRICAL COMPUTER ENG, CLARKSON UNIV, POTSDAM, NY 13676, USA

SO Electrophoresis, (1990) Vol. 11, No. 5, pp. 415-419.

CODEN: ELCTDN. ISSN: 0173-0835.

DT Article

FS BA

LA ENGLISH

ED Entered STN: 21 Aug 1990

Last Updated on STN: 21 Aug 1990

AB This paper reviews th CLIP image processing system for the complete analysis of two-dimensional electrophoresis images. The analysis problem for two-dimensional gel images can be broken down into three issues: segmentation of individual gel images, alignment and comparison of pairs of gel images, and information storage and retrieval. This paper describes these problems and reviews how the CLIP system handles each of them. Segmentation is the location and isolation of each protein spot on an individual gel image and also the extraction of individual spot data such as position, area and volume. There are three basic stages; background field correction, noise filtering, spot detection and information extraction. Alignment and comparison of gel images involves matching protein spots between two gels. This can be quite difficult because there is not a simple relationship which can transform one gel image onto another. The database issues concern storing all the information which has been obtained from the above operations such that retrieval of this information can be readily performed. The advantage of the CLIP system over others is speed of processing. CLIP series computers use one processor for every pixel of the camera image such that image processing algorithms run in parallel. The main disadvantage is in the cost of these machines. With the declining trend in the cost of parallel processors, these machines will become more and more viable alternatives. This paper reviews the algorithms for the analysis of two-dimensional gels. It is shown that CLIP is flexible enough to perform more than one type of algorithm for a particular operation.

CC General biology - Information, documentation, retrieval and computer applications 00530

Mathematical biology and statistical methods 04500

Biochemistry methods - Proteins, peptides and amino acids 10054

Biochemistry studies - Proteins, peptides and amino acids 10064

Biophysics - Methods and techniques 10504

Biophysics - Molecular properties and macromolecules 10506

IT Major Concepts

Biochemistry and Molecular Biophysics; Computer Applications  
(Computational Biology); Mathematical Biology (Computational Biology);  
Methods and Techniques

IT Miscellaneous Descriptors

PROTEIN ANALYSIS COMPUTER APPLICATIONS

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DT Article  
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AB This paper reviews th CLIP image processing system for the complete  
 analysis of two-dimensional electrophoresis images. The analysis problem  
 for two-dimensional gel images can be broken  
 down into three issues: segmentation of individual gel images, alignment  
 and comparison of pairs of gel images, and information storage and  
 retrieval. This paper describes these problems and reviews how the CLIP  
 system handles each of them. Segmentation is the location and isolation  
 of each protein spot on an individual gel image and also the extraction of  
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 Mathematical biology and statistical methods 04500  
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 Biochemistry studies - Proteins, peptides and amino acids 10064  
 Biophysics - Methods and techniques 10504  
 Biophysics - Molecular properties and macromolecules 10506

IT Major Concepts  
 Biochemistry and Molecular Biophysics; Computer Applications  
 (Computational Biology); Mathematical Biology (Computational Biology);  
 Methods and Techniques

IT Miscellaneous Descriptors  
 PROTEIN ANALYSIS COMPUTER APPLICATIONS